



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/607,142A

DATE: 08/28/2002
TIME: 16:13:49

Input Set : N:\Crf3\RULE60\09607142A.RAW
Output Set: N:\CRF4\08282002\I607142A.raw

#13

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TECH CENTER 1600/2900

ENTERED

1 <110> APPLICANT: Cherry, Joel
2 Svendsen, Allan
3 Andersen, Carsten
4 Beier, Lars
5 Frandsen, Torben
6 <120> TITLE OF INVENTION: Maltogenic Alpha-Amylase Variants
7 <130> FILE REFERENCE: 5443.414-US
8 <140> CURRENT APPLICATION NUMBER: 09/607,142A
9 <141> CURRENT FILING DATE: 2000-06-29
11 <150> PRIOR APPLICATION NUMBER: US/09/386,607
12 <151> PRIOR FILING DATE: 1999-08-31
14 <150> PRIOR APPLICATION NUMBER: DK98/00269
15 <151> PRIOR FILING DATE: 1998-02-27
16 <150> PRIOR APPLICATION NUMBER: 60/077,795
17 <151> PRIOR FILING DATE: 1998-03-12
18 <160> NUMBER OF SEQ ID NOS: 14
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2160
23 <212> TYPE: DNA
24 <213> ORGANISM: Bacillus sp.
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(2160)
28 <220> FEATURE:
29 <221> NAME/KEY: mat_peptide
30 <222> LOCATION: (100)..(2157)
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33 Met Lys Lys Lys Thr Leu Ser Leu Phe Val Gly Leu Met Leu Leu Ile
W--> 34 -30 -25 -20
35 ggt ctt ctg ttc agc ggt tct ctt ccg tac aat cca aac gcc gct gaa 96
36 Gly Leu Leu Phe Ser Gly Ser Leu Pro Tyr Asn Pro Asn Ala Ala Glu
W--> 37 -15 -10 -5
38 gcc agc agt tcc gca agc gtc aaa ggg gac gtg att tac cag att atc 144
39 Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile
40 -1 1 5 10 15
41 att gac cgg ttt tac gat ggg gac acg acg aac aac aat cct gcc aaa 192
42 Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys
43 20 25 30
44 agt tat gga ctt tac gat ccg acc aaa tcg aag tgg aaa atg tat tgg 240
45 Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp
46 35 40 45

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47	ggc ggg gat ctg gag ggg gtt cgt caa aaa ctt cct tat ctt aaa cag	288
48	Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln	
49	50 55 60	
50	ctg ggc gta acg aca atc tgg ttg tcc ccg gtt ttg gac aat ctg gat	336
51	Leu Gly Val Thr Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp	
52	65 70 75	
53	aca ctg gcg ggc acc gat aac acg ggc tat cac gga tac tgg acg cgc	384
54	Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg	
55	80 85 90 95	
56	gat ttt aaa cag att gag gaa cat ttc ggg aat tgg acc aca ttt gac	432
57	Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp	
58	100 105 110	
59	acg ttg gtc aat gat gct cac caa aac gga atc aag gtg att gtc gac	480
60	Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp	
61	115 120 125	
62	ttt gtg ccc aat cat tcg act cct ttt aag gca aac gat tcc acc ttt	528
63	Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe	
64	130 135 140	
65	gcg gaa ggc ggc gcc ctc tac aac aat gga acc tat atg ggc aat tat	576
66	Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr	
67	145 150 155	
68	ttt gat gac gca aca aaa ggg tac ttc cac cat aat ggg gac atc agc	624
69	Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser	
70	160 165 170 175	
71	aac tgg gac gac cgg tac gag gcg caa tgg aaa aac ttc acg gat cca	672
72	Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro	
73	180 185 190	
74	gcc ggt ttc tcg ctt gcc gat ttg tcg cag gaa aat ggc acg att gct	720
75	Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala	
76	195 200 205	
77	caa tac ctg acc gat gcg gcg gtt caa ttg gta gca cat gga gcg gat	768
78	Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp	
79	210 215 220	
80	ggt ttg cgg att gat gcg gtg aag cat ttt aat tcg ggg ttc tcc aaa	816
81	Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys	
82	225 230 235	
83	tcg ttg gcc gat aaa ctg tac caa aag aaa gac att ttc ctg gtg ggg	864
84	Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly	
85	240 245 250 255	
86	gaa tgg tac gga gat gac ccc gga aca gcc aat cat ctg gaa aag gtc	912
87	Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val	
88	260 265 270	
89	cgg tac gcc aac aac agc ggt gtc aat gtg ctg gat ttt gat ctc aac	960
90	Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn	
91	275 280 285	
92	acg gtg att cga aat gtg ttc ggc aca ttt acg caa acg atg tac gat	1008
93	Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp	
94	290 295 300	
95	ctt aac aat atg gtg aac caa acg ggg aac gag tac aaa tac aaa gaa	1056

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96	Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu	
97	305 310 315	
98	aat cta atc aca ttt atc gat aac cat gat atg tca aga ttt ctt tcg	1104
99	Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser	
100	320 325 330 335	
101	gta aat tcg aac aag gcg aat ttg cac cag gcg ctt gct ttc att ctc	1152
102	Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu	
103	340 345 350	
104	act tcg cgg ggt acg ccc tcc atc tat tat gga acc gaa caa tac atg	1200
105	Thr Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met	
106	355 360 365	
107	gca ggc ggc aat gac ccg tac aac cgg ggg atg atg ccg gcg ttt gat	1248
108	Ala Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp	
109	370 375 380	
110	acg aca acc acc gcc ttt aaa gag gtg tca act ctg gcg ggg ttg cgc	1296
111	Thr Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg	
112	385 390 395	
113	agg aac aat gcg gcg atc cag tac ggc acc acc acc cag cgt tgg atc	1344
114	Arg Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile	
115	400 405 410 415	
116	aac aat gat gtt tac att tat gaa cgg aaa ttt ttc aac gat gtc gtg	1392
117	Asn Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val	
118	420 425 430	
119	ttg gtg gcc atc aat cga aac acg caa tcc tcc tat tcg att tcc ggt	1440
120	Leu Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly	
121	435 440 445	
122	ttg cag acg gcc ttg cca aat ggc agc tat gcg gat tat ctg tca ggg	1488
123	Leu Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly	
124	450 455 460	
125	ctg ttg ggg ggg aac ggg att tcc gtt tcc aat gga agt gtc gct tcg	1536
126	Leu Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser	
127	465 470 475	
128	ttc acg ctt gcg cct gga gcc gtg tct gtt tgg cag tac agc aca tcc	1584
129	Phe Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser	
130	480 485 490 495	
131	gct tca gcg ccg caa atc gga tcg gtt gct cca aat atg ggg att ccg	1632
132	Ala Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro	
133	500 505 510	
134	ggt aat gtg gtc acg atc gac ggg aaa ggt ttt ggg acg acg cag gga	1680
135	Gly Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly	
136	515 520 525	
137	acc gtg aca ttt ggc gga gtg aca gcg act gtg aaa tcc tgg aca tcc	1728
138	Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser	
139	530 535 540	
140	aat cgg att gaa gtg tac gtt ccc aac atg gcc gcc ggg ctg acc gat	1776
141	Asn Arg Ile Glu Val Tyr Val Pro Asn Met Ala Ala Gly Leu Thr Asp	
142	545 550 555	
143	gtg aaa gtc acc gcg ggt gga gtt tcc agc aat ctg tat tct tac aat	1824
144	Val Lys Val Thr Ala Gly Gly Val Ser Ser Asn Leu Tyr Ser Tyr Asn	

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145      560      565      570      575
146 att ttg agt gga acg cag aca tcg gtt gtg ttt act gtg aaa agt gcg 1872
147 Ile Leu Ser Gly Thr Gln Thr Ser Val Val Phe Thr Val Lys Ser Ala
148      580      585      590
149 cct ccg acc aac ctg ggg gat aag att tac ctg acg ggc aac ata ccg 1920
150 Pro Pro Thr Asn Leu Gly Asp Lys Ile Tyr Leu Thr Gly Asn Ile Pro
151      595      600      605
152 gaa ttg ggg aat tgg agc acg gat acg agc gga gcc gtt aac aat gcg 1968
153 Glu Leu Gly Asn Trp Ser Thr Asp Thr Ser Gly Ala Val Asn Asn Ala
154      610      615      620
155 caa ggg ccc ctg ctc gcg ccc aat tat ccg gat tgg ttt tat gta ttc 2016
156 Gln Gly Pro Leu Leu Ala Pro Asn Tyr Pro Asp Trp Phe Tyr Val Phe
157      625      630      635
158 agc gtt cca gca gga aag acg att caa ttc aag ttc ttc atc aag cgt 2064
159 Ser Val Pro Ala Gly Lys Thr Ile Gln Phe Lys Phe Phe Ile Lys Arg
160      640      645      650      655
161 gcg gat gga acg att caa tgg gag aat ggt tcg aac cac gtg gcc aca 2112
162 Ala Asp Gly Thr Ile Gln Trp Glu Asn Gly Ser Asn His Val Ala Thr
163      660      665      670
164 act ccc acg ggt gca acc ggt aac att act gtt acg tgg caa aac tag 2160
165 Thr Pro Thr Gly Ala Thr Gly Asn Ile Thr Val Thr Trp Gln Asn
166      675      680      685
168 <210> SEQ ID NO: 2
169 <211> LENGTH: 719
170 <212> TYPE: PRT
171 <213> ORGANISM: Bacillus sp.
172 <400> SEQUENCE: 2
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176      20      25      30
177 Ala Ser Ser Ser Ala Ser Val Lys Gly Asp Val Ile Tyr Gln Ile Ile
178      35      40      45
179 Ile Asp Arg Phe Tyr Asp Gly Asp Thr Thr Asn Asn Asn Pro Ala Lys
180      50      55      60
181 Ser Tyr Gly Leu Tyr Asp Pro Thr Lys Ser Lys Trp Lys Met Tyr Trp
182      65      70      75      80
183 Gly Gly Asp Leu Glu Gly Val Arg Gln Lys Leu Pro Tyr Leu Lys Gln
184      85      90      95
185 Leu Gly Val Thr Ile Trp Leu Ser Pro Val Leu Asp Asn Leu Asp
186      100      105      110
187 Thr Leu Ala Gly Thr Asp Asn Thr Gly Tyr His Gly Tyr Trp Thr Arg
188      115      120      125
189 Asp Phe Lys Gln Ile Glu Glu His Phe Gly Asn Trp Thr Thr Phe Asp
190      130      135      140
191 Thr Leu Val Asn Asp Ala His Gln Asn Gly Ile Lys Val Ile Val Asp
192      145      150      155      160
193 Phe Val Pro Asn His Ser Thr Pro Phe Lys Ala Asn Asp Ser Thr Phe
194      165      170      175

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195 Ala Glu Gly Gly Ala Leu Tyr Asn Asn Gly Thr Tyr Met Gly Asn Tyr
196                      180                      185                      190
197 Phe Asp Asp Ala Thr Lys Gly Tyr Phe His His Asn Gly Asp Ile Ser
198                      195                      200                      205
199 Asn Trp Asp Asp Arg Tyr Glu Ala Gln Trp Lys Asn Phe Thr Asp Pro
200                      210                      215                      220
201 Ala Gly Phe Ser Leu Ala Asp Leu Ser Gln Glu Asn Gly Thr Ile Ala
202                      225                      230                      235                      240
203 Gln Tyr Leu Thr Asp Ala Ala Val Gln Leu Val Ala His Gly Ala Asp
204                      245                      250                      255
205 Gly Leu Arg Ile Asp Ala Val Lys His Phe Asn Ser Gly Phe Ser Lys
206                      260                      265                      270
207 Ser Leu Ala Asp Lys Leu Tyr Gln Lys Lys Asp Ile Phe Leu Val Gly
208                      275                      280                      285
209 Glu Trp Tyr Gly Asp Asp Pro Gly Thr Ala Asn His Leu Glu Lys Val
210                      290                      295                      300
211 Arg Tyr Ala Asn Asn Ser Gly Val Asn Val Leu Asp Phe Asp Leu Asn
212                      305                      310                      315                      320
213 Thr Val Ile Arg Asn Val Phe Gly Thr Phe Thr Gln Thr Met Tyr Asp
214                      325                      330                      335
215 Leu Asn Asn Met Val Asn Gln Thr Gly Asn Glu Tyr Lys Tyr Lys Glu
216                      340                      345                      350
217 Asn Leu Ile Thr Phe Ile Asp Asn His Asp Met Ser Arg Phe Leu Ser
218                      355                      360                      365
219 Val Asn Ser Asn Lys Ala Asn Leu His Gln Ala Leu Ala Phe Ile Leu
220                      370                      375                      380
221 Thr Ser Arg Gly Thr Pro Ser Ile Tyr Tyr Gly Thr Glu Gln Tyr Met
222                      385                      390                      395                      400
223 Ala Gly Gly Asn Asp Pro Tyr Asn Arg Gly Met Met Pro Ala Phe Asp
224                      405                      410                      415
225 Thr Thr Thr Thr Ala Phe Lys Glu Val Ser Thr Leu Ala Gly Leu Arg
226                      420                      425                      430
227 Arg Asn Asn Ala Ala Ile Gln Tyr Gly Thr Thr Thr Gln Arg Trp Ile
228                      435                      440                      445
229 Asn Asn Asp Val Tyr Ile Tyr Glu Arg Lys Phe Phe Asn Asp Val Val
230                      450                      455                      460
231 Leu Val Ala Ile Asn Arg Asn Thr Gln Ser Ser Tyr Ser Ile Ser Gly
232                      465                      470                      475                      480
233 Leu Gln Thr Ala Leu Pro Asn Gly Ser Tyr Ala Asp Tyr Leu Ser Gly
234                      485                      490                      495
235 Leu Leu Gly Gly Asn Gly Ile Ser Val Ser Asn Gly Ser Val Ala Ser
236                      500                      505                      510
237 Phe Thr Leu Ala Pro Gly Ala Val Ser Val Trp Gln Tyr Ser Thr Ser
238                      515                      520                      525
239 Ala Ser Ala Pro Gln Ile Gly Ser Val Ala Pro Asn Met Gly Ile Pro
240                      530                      535                      540
241 Gly Asn Val Val Thr Ile Asp Gly Lys Gly Phe Gly Thr Thr Gln Gly
242                      545                      550                      555                      560
243 Thr Val Thr Phe Gly Gly Val Thr Ala Thr Val Lys Ser Trp Thr Ser

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09607142A.RAW

Output Set: N:\CRF4\08282002\I607142A.raw

L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

L:37 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1